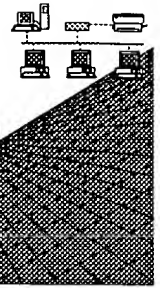


C. Kaufman

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



# **RAW SEQUENCE LISTING**

## **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following CRF diskette:

Application Serial Number: 09/157,289A  
Art Unit / Team No. : 1646  
Date Processed by STIC: 6/14/99

**THE ATTACHED PRINTOUT EXPLAINS THE ERRORS DETECTED.**

**PLEASE BE SURE TO FORWARD THIS INFORMATION TO THE APPLICANTS BY EITHER:**

**1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANTS ALONG WITH A NOTICE TO COMPLY or,**

**2) CALLING APPLICANTS AND FAXING THEM A COPY OF THE PRINTOUT WITH A NOTICE TO COMPLY**

**THIS WILL INSURE THAT THE NEXT SUBMISSION RECEIVED FROM THEM WILL BE ERROR FREE.**

**IF YOU HAVE ANY FURTHER QUESTIONS, PLEASE CALL:**

**ARTI SHAH 703-308-4212**

# Raw Sequence Listing Error Summary

## ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/157,289A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics      The number/text at the end of each line "wrapped" down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2        Wrapped Aminos      The amino acid number/text at the end of each line "wrapped " down to the next line.  
This may occur if your file was retrieved in a word processor after creating it.  
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3        Incorrect Line Length      The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4        Misaligned Amino Acid      The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs  
Numbering      between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5        Non-ASCII      This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.  
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6        Variable Length      Sequence(s)        contain n's or Xaa's which represented more than one residue.  
As per the rules, each n or Xaa can only represent a single residue.  
Please present the maximum number of each residue having variable length and  
indicate in the (ix) feature section that some may be missing.
- 7        PatentIn ver. 2.0 "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid  
sequence(s)       . Normally, PatentIn would automatically generate this section from the  
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section  
to the subsequent amino acid sequence.
- 8        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence:  
(OLD RULES)      (2) INFORMATION FOR SEQ ID NO:X:  
                                 (1) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")  
                                 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:  
                                 This sequence is intentionally skipped  
  
Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9        Skipped Sequences      Sequence(s)        missing. If intentional, please use the following format for each skipped sequence.  
(NEW RULES)      <210> sequence id number  
                                 <400> sequence id number  
                                 000
- 10        Use of n's or Xaa's      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if n's or Xaa's are present.  
                                 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11        Use of <213>Organism      Sequence(s)        are missing this mandatory field or its response.  
(NEW RULES)
- 12        Use of <220>Feature      Sequence(s)        are missing the <220>Feature and associated headings.  
(NEW RULES)      Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"  
                                 Please explain source of genetic material in <220> to <223> section.  
                                 (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)      (Sec. 1.823 of new Rules)
- 13        PatentIn ver. 2.0 "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted  
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).  
Instead, please use "File Manager" or any other means to copy file to floppy disk.

Important

PAGE: 1

RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/157,289ADATE: 06/14/1999  
TIME: 15:31:19

Input Set: I157289A.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

1 <110> APPLICANT: ASHKENAZI, AVI J.  
2 BOTSTEIN, DAVID  
3 DODGE, KELLY H.  
4 GURNEY, AUSTIN L.  
5 KIM, KYUNG JIN  
6 LAWRENCE, DAVID A.  
7 PITTI, ROBERT  
8 ROY, MARGARET A.  
9 TUMAS, DANIEL B.  
10 WOOD, WILLIAM I.  
11 GENENTECH INC.  
12 <120> TITLE OF INVENTION: DcR3 Polypeptide, A TNFR Homolog  
13 <130> FILE REFERENCE: 11669.31US03  
14 <140> CURRENT APPLICATION NUMBER: US/09/157,289A  
15 <141> CURRENT FILING DATE: 1998-09-18  
16 <150> EARLIER APPLICATION NUMBER: 60/059,288  
17 <151> EARLIER FILING DATE: 1997-09-18  
18 <150> EARLIER APPLICATION NUMBER: 60/094,640  
19 <151> EARLIER FILING DATE: 1998-07-30  
20 <160> NUMBER OF SEQ ID NOS: 16  
21 <170> SOFTWARE: PatentIn Ver. 2.0  
22 <210> SEQ ID NO 1  
23 <211> LENGTH: 300  
24 <212> TYPE: PRT  
25 <213> ORGANISM: Homo sapiens  
26 <400> SEQUENCE: 1  
27 Met Arg Ala Leu Glu Gly Pro Gly Leu Ser Leu Leu Cys Leu Val Leu  
28 1 5 10 15  
29 Ala Leu Pro Ala Leu Leu Pro Val Pro Ala Val Arg Gly Val Ala Glu  
30 20 25 30  
31 Thr Pro Thr Tyr Pro Trp Arg Asp Ala Glu Thr Gly Glu Arg Leu Val  
32 35 40 45  
33 Cys Ala Gln Cys Pro Pro Gly Thr Phe Val Gln Arg Pro Cys Arg Arg  
34 50 55 60  
35 Asp Ser Pro Thr Thr Cys Gly Pro Cys Pro Pro Arg His Tyr Thr Gln  
36 65 70 75 80  
37 Phe Trp Asn Tyr Leu Glu Arg Cys Arg Tyr Cys Asn Val Leu Cys Gly  
38 85 90 95  
39 Glu Arg Glu Glu Glu Ala Arg Ala Cys His Ala Thr His Asn Arg Ala  
40 100 105 110  
41 Cys Arg Cys Arg Thr Gly Phe Phe Ala His Ala Gly Phe Cys Leu Glu  
42 115 120 125  
43 His Ala Ser Cys Pro Pro Gly Ala Gly Val Ile Ala Pro Gly Thr Pro  
44 130 135 140

Does Not Comply  
Corrected Diskette Needed

ppr. 2-4

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RAW SEQUENCE LISTING  
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Input Set: I157289A.RAW

45 Ser Gln Asn Thr Gln Cys Gln Pro Cys Pro Pro Gly Thr Phe Ser Ala  
46 145 150 155 160  
47 Ser Ser Ser Ser Ser Glu Gln Cys Gln Pro His Arg Asn Cys Thr Ala  
48 165 170 175  
49 Leu Gly Leu Ala Leu Asn Val Pro Gly Ser Ser Ser His Asp Thr Leu  
50 180 185 190  
51 Cys Thr Ser Cys Thr Gly Phe Pro Leu Ser Thr Arg Val Pro Gly Ala  
52 195 200 205  
53 Glu Glu Cys Glu Arg Ala Val Ile Asp Phe Val Ala Phe Gln Asp Ile  
54 210 215 220  
55 Ser Ile Lys Arg Leu Gln Arg Leu Leu Gln Ala Leu Glu Ala Pro Glu  
56 225 230 235 240  
57 Gly Trp Gly Pro Thr Pro Arg Ala Gly Arg Ala Ala Leu Gln Leu Lys  
58 245 250 255  
59 Leu Arg Arg Arg Leu Thr Glu Leu Leu Gly Ala Gln Asp Gly Ala Leu  
60 260 265 270  
61 Leu Val Arg Leu Leu Gln Ala Leu Arg Val Ala Arg Met Pro Gly Leu  
62 275 280 285  
63 Glu Arg Ser Val Arg Glu Arg Phe Leu Pro Val His  
64 290 295 300

65 <210> SEQ ID NO 2  
66 <211> LENGTH: 1114  
67 <212> TYPE: DNA  
68 <213> ORGANISM: Homo sapiens  
69 <220> FEATURE:  
70 <223> OTHER INFORMATION: @ nt 1090  
71 <400> SEQUENCE: 2

*Please see item 10 on  
Enr summary sheet  
what does this mean?*

72 tccgcaggcg gaccgggggc aaaggaggtg gcatgtcggg caggcacagc agggctcctgt 60  
73 gtccgcgctg agccgcgctc tcctgtctcc agcaaggacc atgagggcgc tggagggggc 120  
74 aggcctgtcg ctgctgtgcc tgggtgtggc gctgcctgcc ctgctgccgg tgcgggctgt 180  
75 acgcggagtg gcagaaacac ccacctaccc ctggcgggac gcagagacag gggagcggct 240  
76 ggtgtgcgcc cagtgcctcc caggcacctt tgtgcagcgg ccgtgccgcc gagacagccc 300  
77 cagcagctgt ggcccgtgtc caccgcgcc ctacacgcag ttctggaact acctggagcg 360  
78 ctgccgtac tgcaacgtcc tctgcgggga gcgtgaggag gaggcacggg cttgccacgc 420  
79 caccacaac cgtgcctgcc gctgccgcac cggcttcttc gcgcacgctg gtttctgctt 480  
80 ggagcacgca tcgtgtccac ctggtgccgg cgtgattgcc ccgggcaccc ccagccagaa 540  
81 cagcagtgcc cagccgtgcc ccccaggcac cttctcagcc agcagctcca gctcagagca 600  
82 gtgccagccc caccgcaact gcacggccct gggcctggcc ctcaatgtgc caggctcttc 660  
83 ctcccatgac accctgtgca ccagctgcac tggcttcccc ctacagacca gggtagcagg 720  
84 agctgaggag tgtgagcgtg ccgtcatcga ctttgtggct ttccaggaca tctccatcaa 780  
85 gaggtgcag cggctgctgc aggcctcga gggcccgagg ggctggggtc cgacaccaag 840  
86 gggggggcgc ggggccttgc agctgaagct gcgtcgccgg ctcacggagc tcctgggggc 900  
87 gcaggacggg gcgctgctgg tgcggctgct gcaggcgctg cgcgtggcca ggatgcccgg 960  
88 gctggagcgg agcgtccgtg agcgttctc ccctgtgcac tgatcctggc cccctcttat 1020  
89 ttattctaca tccttggcac ccacttgca ctgaaagagg ctttttttta aatagaagaa 1080  
90 atgaggtttt ttaaaaaaaaa aaaaaaaaaa aaaa 1114

W--&gt;

91 <210> SEQ ID NO 3  
92 <211> LENGTH: 491  
93 <212> TYPE: DNA  
94 <213> ORGANISM: Unknown

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/157,289A

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Input Set: I157289A.RAW

95 <220> FEATURE:  
96 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN  
97 <220> FEATURE:  
98 <223> OTHER INFORMATION: 61, 73, 86, 98 *what does "n" represent at these locations?*  
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W--> 101 antaactgga gcñctgccgc tactgnaacg tcctctgngg ggagcgtgag gaggaggcac 120  
102 gggcttgcca cgccaccac aaccgtgcct gccgctgccg caccggcttc ttgcgcacg 180  
103 ctggtttctg cttggagcac gcatcgtgtc cacctggtgc cggcgtgatt gccccgggca 240  
104 cccccagcca gaacacgcag tgcctagccg tgccccccag gcaccttctc agccagcagc 300  
105 tccagctcag agcagtgccg gccccaccgc aactgcacgg ccctgggcct ggccctcaat 360  
106 gtgccaggct cttcctccca tgacaccctg tgcaccagct gcactggctt cccctcagc 420  
107 accaggttac caggagctga ggagtgtgag cgtgccgtca tcgactttgt ggctttccag 480  
108 gacatctcca t 491  
109 <210> SEQ ID NO 4  
110 <211> LENGTH: 73  
111 <212> TYPE: DNA  
112 <213> ORGANISM: Unknown  
113 <220> FEATURE:  
114 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN  
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117 ctacctggag cgc 73  
118 <210> SEQ ID NO 5  
119 <211> LENGTH: 271  
120 <212> TYPE: DNA  
121 <213> ORGANISM: Unknown  
122 <220> FEATURE:  
123 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN  
124 <220> FEATURE:  
125 <223> OTHER INFORMATION: 52, 62, 73, 86, 98, 106, 120, 121, 153, 167, 184, *what does "n" represent?*  
126 220 and 233  
127 <400> SEQUENCE: 5  
W--> 128 gccgagacag ccccacgacg tgtggcccgt gtccaccgcg ccactacacg cagttctgga 60  
W--> 129 antaactgga gcñctgccgc tactgnaacg tcctctgngg ggagcgtgag gaggaggcan 120  
W--> 130 ggccttgcca cgccaccac aaccgcgcct gcñgctgcag caccggnttc ttgcgcacg 180  
W--> 131 ctgntttctg cttggagcac gcatcgtgtc cacctggtgn cggcgtgatt gcñccgggca 240  
132 cccccagcca gaacacgcag gcaaagccgt g 271  
133 <210> SEQ ID NO 6  
134 <211> LENGTH: 201  
135 <212> TYPE: DNA  
136 <213> ORGANISM: Unknown  
137 <220> FEATURE:  
138 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN  
139 <220> FEATURE:  
140 <223> OTHER INFORMATION: 182 *what does "n" represent?*  
141 <400> SEQUENCE: 6  
142 gcagttctgg aactacctgg agcgtgccg ctactgcaac gtcctctgcg gggagcgtga 60  
143 ggaggaggca cgggcttgcc acgccacca caaccgtgcc tgccgctgcc gcaccggctt 120  
144 cttgcgcac gctggtttct gcttgagca cgcacgtgt ccacctggtg cggcgctgat 180

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/157,289A

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Input Set: I157289A.RAW

W--> 145 tnccccgggc acccccagcc a 201  
146 <210> SEQ ID NO 7  
147 <211> LENGTH: 277  
148 <212> TYPE: DNA  
149 <213> ORGANISM: Unknown  
150 <220> FEATURE:  
151 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN  
152 <220> FEATURE:  
153 <223> OTHER INFORMATION: (141) 142 what does "n" represent?  
154 <400> SEQUENCE: 7  
155 gaggggcccc caggagtggg ggccggaggt gtggcagggg tcaggttgct ggtcccagcc 60  
156 ttgcaccctg agctaggaca ccagttcccc tgaccctgtt ctccctcct ggctgcaggg 120  
W--> 157 acccccagcc agaacacgca ggcagccgt gccccccagg caccttctca gccagcagct 180  
158 ccagctcaga gcagtgccag ccccaccgca actgcacggc cctgggctg gccctcaatg 240  
159 tgccaggctc ttctcccat gacacctgt gcaccag 277  
160 <210> SEQ ID NO 8  
161 <211> LENGTH: 199  
162 <212> TYPE: DNA  
163 <213> ORGANISM: Unknown  
164 <220> FEATURE:  
165 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN  
166 <400> SEQUENCE: 8  
167 gcctcgtgtc cacctgtgtc cggcgtgatt gccccgggca ccccagcca gaacacgcag 60  
168 gcctagccgt gccccccagg caccttctca gccagcagct ccagctcaga gcagtgccag 120  
169 ccccaccgca actgcacggc cctgggctg gccctcaatg tgccaggctc ttctcccat 180  
170 gacacctgt gcaccagct 199  
171 <210> SEQ ID NO 9  
172 <211> LENGTH: 226  
173 <212> TYPE: DNA  
174 <213> ORGANISM: Unknown  
175 <220> FEATURE:  
176 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN  
177 <220> FEATURE:  
178 <223> OTHER INFORMATION: 4, 9, 12, 64, 69, 72, 175 165 what does "n" represent?  
179 <400> SEQUENCE: 9  
W--> 180 agccttgcc cccagggcacc ttctcagcca gcagttccag ctccagagcag tgccagcccc 60  
181 accgcaactg caggccctg ggcttgccc tcaatgtgcc aggtcttcc tccatgaca 120  
W--> 182 cgctgtgcac cagctgcact ggcttcccc tcagcaccag ggtanagga gctgaggagt 180  
183 gtgagcgtgc cgtcatcgac tttgtggctt tccaggacat ctccat 226  
184 <210> SEQ ID NO 10  
185 <211> LENGTH: 283  
186 <212> TYPE: DNA  
187 <213> ORGANISM: Homo sapiens  
188 <220> FEATURE:  
189 <223> OTHER INFORMATION: 27, 37, 64, 140 what does "n" represent?  
190 <400> SEQUENCE: 10  
W--> 191 cttggtccacc tgggtgccggc gtgatttccc gggcaccccc agccagaaca cgcagtgcc 60  
W--> 192 gocntcccc caggcacctt ctccagccagc agctccagct cagagcagtg ccagccccac 120  
W--> 193 cgcaactgca acgccctggg ctggccctca atgtgccagg ctcttctctcc catgacaccc 180  
194 tgtgcaccag ctgcactggc ttccccctca gcaccagggt accaggagct gaggagtgtg 240

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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/157,289ADATE: 06/14/1999  
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Input Set: I157289A.RAW

```
195          agcgtgccgt catcgacttt gtggctttcc aggacatctc cat                283
196 <210> SEQ ID NO 11
197 <211> LENGTH: 21
198 <212> TYPE: DNA
199 <213> ORGANISM: Unknown
200 <220> FEATURE:
201 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
202 <400> SEQUENCE: 11
203          cacgctgggtt tctgcttgga g                                21
204 <210> SEQ ID NO 12
205 <211> LENGTH: 22
206 <212> TYPE: DNA
207 <213> ORGANISM: Unknown
208 <220> FEATURE:
209 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
210 <400> SEQUENCE: 12
211          agctgggtgca cagggtgtca tg                                22
212 <210> SEQ ID NO 13
213 <211> LENGTH: 53
214 <212> TYPE: DNA
215 <213> ORGANISM: Unknown
216 <220> FEATURE:
217 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
218 <400> SEQUENCE: 13
219          cccaggcacc ttctcagcca gccagcagct ccagctcaga gcagtgccag ccc        53
220 <210> SEQ ID NO 14
221 <211> LENGTH: 24
222 <212> TYPE: DNA
223 <213> ORGANISM: Unknown
224 <220> FEATURE:
225 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
226 <400> SEQUENCE: 14
227          acacgatgcg tgctccaagc agaa                                24
228 <210> SEQ ID NO 15
229 <211> LENGTH: 17
230 <212> TYPE: DNA
231 <213> ORGANISM: Unknown
232 <220> FEATURE:
233 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
234 <400> SEQUENCE: 15
235          cttcttcgcg cacgctg                                17
236 <210> SEQ ID NO 16
237 <211> LENGTH: 16
238 <212> TYPE: DNA
239 <213> ORGANISM: Unknown
240 <220> FEATURE:
241 <223> OTHER INFORMATION: Description of Unknown Organism: UNKNOWN
242 <400> SEQUENCE: 16
243          atcacgccgg caccag                                16
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Input Set: I157289A.RAW

Line	?	Error/Warning	Original Text
90	W	"N" or "Xaa" used: Feature required	atgaggtttn ttaaaaaaaaaa aaaaaaaaaa aaaa
101	W	"N" or "Xaa" used: Feature required	antaactgga gcnctgccgc tactgnaacg tcctctgn
128	W	"N" or "Xaa" used: Feature required	gccgagacag cccacgacg tgtggcccggt gtccaccg
129	W	"N" or "Xaa" used: Feature required	antaactgga gcnctgccgc tactgnaacg tcctctgn
130	W	"N" or "Xaa" used: Feature required	gngcttgcca cgccaccac aaccgcgcct gcngctgc
131	W	"N" or "Xaa" used: Feature required	ctgntttctg cttggagcac gcatcgtgtc cacctggt
145	W	"N" or "Xaa" used: Feature required	tnccccgggc acccccagcc a
157	W	"N" or "Xaa" used: Feature required	acccccagcc agaacacgca gnccagccgt gcccccca
180	W	"N" or "Xaa" used: Feature required	agcngtgcnc cncaggcacc ttctcagcca gcagttcc
182	W	"N" or "Xaa" used: Feature required	cgctgtgcac cagctgcact ggcttcccc tcagcacc
191	W	"N" or "Xaa" used: Feature required	cttgtccacc tggtgccggc gtgattnccc gggcacc
192	W	"N" or "Xaa" used: Feature required	gcntcccc caggcacctt ctcagccagc agctccag
193	W	"N" or "Xaa" used: Feature required	cgcaactgca acgccctggn ctggccctca atgtgcca